

EXHIBIT B
U.S. Serial No. 09/981,124
Filed: October 17, 2001
Applicants: Allan Green, et al.



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.17 [Aug-26-2007]

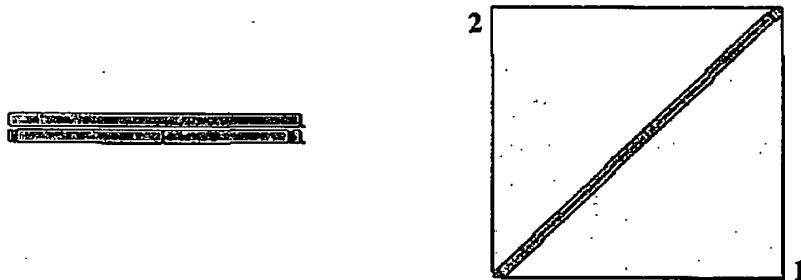
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **0** expect: **10.000** wordsize: **3** Filter View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
 Show CDS translation **Align**

Sequence 1: [gi|5997736|Sequence 2 from patent US 5850026 >gi|20230158|gb|AAE91301.1| Sequence 14 from patent US 6342658 >gi|40193154|gb|AAR78126.1| Sequence 14 from patent US 6649782 >gi|83349266|gb|ABC14919.1| Sequence 14 from patent US 6967243 >gi|160812277|emb|CAP40200.1| unnamed protein product \[Brassica napus\] >gi|162771692|emb|CAP58837.1| unnamed protein product \[Brassica napus\]](#)

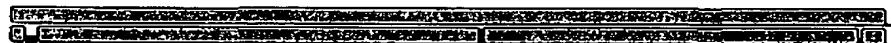
Length = 384 (1 .. 384)

Sequence 2: unnamed protein product

Length = 374 (1 .. 374)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 476 bits (1224), Expect = 3e-132
 Identities = 216/381 (56%), Positives = 279/381 (73%), Gaps = 9/381 (2%)

```

Query 1   MGAGGRMQVSPPSKKSETDTIKRVCETPPFTVGELKKAIPPHCFKRSIPRSFSYLIWDI 60
          MGAGGR      + SE  ++RV      F++ ELK+AIPPHCF+RS+ RS  Y++ ++
Sbjct 1   MGAGGR-----GRTSEKSMERVSVPVTFSLSELKQAIIPPHCFQRSVIRSSYYVVENL 54

Query 61  IIASCFYYVATTYFPLLPPLSYFAWPLYWACQGCVLTVGVVIAHECGHHAFSDYQWLDD 120
          IIA  FY++A TY P LP  L+Y AWP YW CQ  LTG+W++ HECGHHAFS+Y W DD
Sbjct 55  IIAYIFYFLANTYIPTLPTSLAYLAWPKYWFCQASKLTGLWILGHECGHHAFSNTWFD 114

Query 121 TVGLIFHSFLLVPYFSWKYSHRRHHSNTGSLERDEVFVPPKKSDIKWYGKYLNNPLGRTV 180
          TVG I HSFLL PYFSW +SHR HHSNT S++ DEV++PK KS +   K LNNP GR +
    
```

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?>

10/2008

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Sbjct 115 TVGFILHSFLLTPYFSWLFSHRNHHSNTSSIDNDEVYIPKSKSKLARIYKLLNPPGRLL 174

Query 181 MLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHPNAPIYNDRERLQIYISDAGILAVCYGL 240
+L + FTLG+PLYL N+SG+ YD FA HF P +PI+ +RER Q+++SD G+LAV YG+

Sbjct 175 VLIIMFTLGFPLYLLTNISGKKYD-REANHFDPMSPIFKERERFQVFLSDLGLLAVFYGI 233

Query 241 FRYAAAQGVASMVCFYGVPELLIVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDR 300
A +G A + C YGVP+L V F +IT+L HTH S PHYDS+EW+W+RGAL+ +DR

Sbjct 234 KVAVANKGAAWVACMYGVPVLGVETFFDVITFLHHTHQSSPHYDSTEWNWIRGALSAIDR 293

Query 301 DYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPVVKAMWREA 360
D+G LN VFH++T THV HHLFS +PHYHA EA AIKPILG++Y D TP++KAMWRE

Sbjct 294 DFGFLNSVFHDVTHTHVMHHLFSYIPHYHAKEARDAIKPILGDFYIMIDRTPILKAMWREG 353

Query 361 KECIYVEPDRQGEKKGVFWYN 381
+EC+Y+EPD + KGV+WY+

Sbjct 354 RECMYIEPD--SKLKGVYWH 372

CPU time: 0.12 user secs. 0.04 sys. secs 0.16 total secs.

EXHIBIT C
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